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VERIFICATION

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The undersigned declares further that all statements made herein of his/her own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

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PATENT OFFICE

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This is to certify that the annexed is a true copy of the following application as filed with this Office.

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[TITLE OF INVENTION] HUMAN CYCLIN I AND GENES ENCODING SAME

[WHAT IS CLAIMED IS]

[Claim 1]

A polypeptide forming a complex with kinase and controlling the activity of the kinase, said polypeptide comprising within a molecule thereof, at least a part or the whole of the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING.

[Claim 2]

A polypeptide comprising within a molecule thereof, at least the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING.

[Claim 3]

A polypeptide forming a complex with kinase and controlling the activity of the kinase, said polypeptide being a polypeptide according to claim 1 or 2 that has varied or has been induced to vary.

[Claim 4]

A polypeptide forming a complex with kinase and controlling the activity of the kinase, said polypeptide comprising consecutive 100 amino acid residues having 30% or more homology with the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING.

[Claim 5]

A polynucleotide encoding the polypeptide according to any of claims 1 to 4.

[Claim 6]

An antisense polynucleotide corresponding to a polynucleotide having a part or the whole of the base sequence set forth in SEQ ID NO: 2 in SEQUENCE LISTING, said antisense polynucleotide controlling the biosynthesis of the polypeptide according to any of claims 1 to 4.

[Claim 7]

The polynucleotide according to claim 6, said polynucleotide being a polynucleotide that has varied or has been induced to vary.

[Claim 8]

A method for selectively detecting neuron comprising detecting mRNA which is present in said neuron and encodes the polypeptide according to any of claims 1 to 4 by means of a labeled cRNA or cDNA that is complementary to said mRNA.

[Claim 9]

An antibody directed against an antigen having a part or the whole of the polypeptide according to any of clams 1 to 4, said antibody recognizing the polypeptide set forth in SEQ ID NO: 1 in SEQUENCE LISTING.

[Claim 10]

A method for selectively detecting neuron comprising detecting the polypeptide according to any of claims 1 to 4 which is present in the neuron by means of the antibody according to claim 9.

[Claim 11]

A recombinant plasmid comprising the polynucleotide according to claim 5.

[Claim 12]

A microbial cell transformed with the plasmid according to claim 11.

[DETAILED DESCRIPTION OF THE INVENTION]

[0001]

[Technical Field to Which the Invention Belongs]

This invention relates to human cyclin I gene. More specifically, it relates to the polypeptide for human cyclin I and a polynucleotide encoding the polypeptide of the human cyclin I.

[0002]

[Prior Art]

Cyclin is a general term to describe polypeptides that are subunits controlling the activities of cyclin-dependant protein kinase (Cdk) and eight species of cyclin, namely cyclins A-H, have been documented. Cyclin is known to form a complex with Cdk and to exhibit the capability of intracelluar

phosphorylation.

[0003]

Also, structural characteristics in cyclins are that they posses a region called " cyclin box" which comprises about 100 amino acids within portions of their amino acid sequences. It is recognized that the eight species of cyclins hitherto known are provided with a high degree of homology in the amino acid sequences of this cyclin box. Hence, it is believed that binding to Cdk at this cyclin box portion is a step necessary for controlling Cdk.

[0004]

It is also recognized that the ability of cyclins to phosphorylate Cdk plays a critical role in the control of cell proliferation and through their ability cyclins bear close relation to phenomena such as cancer and immunity. Also, it is suggested that some cyclins are widely involved not only in the control of cell cycle, but also in the signal transmission.

[0005]

Accordingly, there is strong likelihood that proteins having a significant homology in the amino acid sequence for the region known as cyclin box are cyclins. In this case, it is therefore anticipated that the proteins have the binding ability to Cdk and

further that they have the ability to control kinase. See, Experimental Medicine, vol. 13, No. 6 (special issue), 1995.

[0006]

[Problems to be Solved by the Invention]

The discovery and identification of novel cyclins enables their use in elucidation of the detailed control mechanism of Cdk by cyclins as well as in the control of cell proliferation among others on the basis of the finding thus obtained. Further, it is thought that the elucidation of novel cyclin with regard to variation of its quantity, its localization, its activation or the like within the cells brings knowledge useful to develop effective methods for the treatment of cancer or immune disorders, therapeutic agents therefor, methods for its diagnosis, diagnostic agents therefor, etc. Therefore, discovery and identification of novel cyclins is strongly demanded.

[0007]

It is one object of this invention to discover and identify a novel cyclin. A further object of the invention is to determine the amino acid sequence of the cyclin and to characterize a gene encoding the cyclin.

[0008]

Also, it is an object of the invention to provide

an expression vector into which the gene of the cyclin is incorporated, a transformant into which the expression vector is introduced, and a recombinant protein obtained by growing the transformants.

[0009]

Also, it is an object of the invention to provide a novel neuron marker based on the protein.

[0010]

Further, it is another object of the invention to provide a method for detecting the cyclin using the antisera of the cyclin.

[0011]

[Means for Solving the Problems]

As a result of thorough investigations with an aim to achieving the aforementioned objects, the present inventor has extensively screened a gene encoding a protein present in human brain cells and succeeded in isolating a gene encoding cyclin-like polypeptide which has an amino acid sequence with a high degree of homology to the amino acid sequence for the known cyclin box. This gene will be herein referred to as " human cyclin I gene" and the protein encoded by this gene referred to as " human cyclin I." Further, the present inventor has succeeded in producing the recombinant cyclin I protein in large quantities by incorporating the isolated human cyclin I gene into an

expression vector and introducing the expression vector into *E. coli* cells and have thus accomplished the invention.

[0012]

Still further, the present inventor has developed a novel, simple method for selectively detecting neuron by using the thus obtained human cyclin I and a gene thereof.

[0013]

Also, the present inventor has succeeded in preparing anti-human cyclin I sera directed against the antigen that is the human cyclin protein.

[0014]

More specifically, this invention provides a polypeptide forming a complex with kinase and controlling the activity of the kinase, said polypeptide comprising within a molecule thereof, at least a part or the whole of the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING.

[0015]

Further, the invention provides a polypeptide comprising within a molecule thereof, at least the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING.

[0016]

Also, the invention provides a polypeptide

forming a complex with kinase and controlling the activity of the kinase, said polypeptide comprising within a molecule thereof, at least a part or the whole of the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING that has varied or has been induced to vary, or comprising within a molecule thereof, at least the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING that has varied or has been induced to vary.

[0017]

Also, the invention provides a polypeptide forming a complex with kinase and controlling the activity of the kinase, said polypeptide comprising consecutive 100 amino acid residues having 30% or more homology with the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING.

[0018]

Further, the invention provides a polynucleotide encoding any of the following polypeptides forming a complex with kinase and controlling the activity of the kinase:

a polypeptide comprising within a molecule thereof, at least a part or the whole of the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING;

a polypeptide comprising within a molecule thereof,

at least the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING;

a polypeptide comprising within a molecule thereof, at least a part or the whole of the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING that has varied or has been induced to vary;

a polypeptide comprising within a molecule thereof, at least the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING that has varied or has been induced to vary; or

a polypeptide comprising consecutive 100 amino acid residues having 30% or more homology with the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING.

[0019]

Additionally, the invention provides an antisense polynucleotide corresponding to a polynucleotide having a part or the whole of the base sequence set forth in SEQ ID NO: 2 in SEQUENCE LISTING, said antisense polynucleotide controlling the biosynthesis of any of the following polypeptides forming a complex with kinase and controlling the activity of the kinase:

a polypeptide comprising within a molecule thereof, at least a part or the whole of the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING;

a polypeptide comprising within a molecule thereof, at least the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING;

a polypeptide comprising within a molecule thereof, at least a part or the whole of the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING that has varied or has been induced to vary;

a polypeptide comprising within a molecule thereof, at least the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING that has varied or has been induced to vary; or

a polypeptide comprising consecutive 100 amino acid residues having 30% or more homology with the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING.

[0020]

Further, the invention provides the aforementioned polynucleotide that has varied or has been induced to vary.

[0021]

Also, the invention provides a method for selectively detecting neuron comprising detecting mRNA which is present in said neuron and encodes any of the following polypeptides forming a complex with kinase and controlling the activity of the kinase, by means of a labeled cRNA or cDNA that is complementary to

said mRNA:

a polypeptide comprising within a molecule thereof, at least a part or the whole of the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING;

a polypeptide comprising within a molecule thereof, at least the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING;

a polypeptide comprising within a molecule thereof, at least a part or the whole of the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING that has varied or has been induced to vary;

a polypeptide comprising within a molecule thereof, at least the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING that has varied or has been induced to vary; or

a polypeptide comprising consecutive 100 amino acid residues having 30% or more homology with the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING.

[0022]

In addition, the invention provides an antibody directed against an antigen having a part or the whole of any of the following polypeptides forming a complex with kinase and controlling the activity of the kinase, said antibody recognizing the polypeptide set forth in

SEQ ID NO: 1 in SEQUENCE LISTING:

a polypeptide comprising within a molecule thereof, at least a part or the whole of the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING;

a polypeptide comprising within a molecule thereof, at least the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING;

a polypeptide comprising within a molecule thereof, at least a part or the whole of the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING that has varied or has been induced to vary;

a polypeptide comprising within a molecule thereof, at least the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING that has varied or has been induced to vary; or

a polypeptide comprising consecutive 100 amino acid residues having 30% or more homology with the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING.

[0023]

Furthermore, the invention provides a method for selectively detecting neuron comprising detecting any of the following polypeptides forming a complex with kinase and controlling the activity of the kinase, which is present in the neuron;

a polypeptide comprising within a molecule thereof, at least a part or the whole of the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING;

a polypeptide comprising within a molecule thereof, at least the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING;

a polypeptide comprising within a molecule thereof, at least a part or the whole of the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING that has varied or has been induced to vary;

a polypeptide comprising within a molecule thereof, at least the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING that has varied or has been induced to vary; or

a polypeptide comprising consecutive 100 amino acid residues having 30% or more homology with the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING;

by means of a antibody directed against an antigen having a part or the whole of any of the following polypeptides;

a polypeptide comprising within a molecule thereof, at least a part or the whole of the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING;

a polypeptide comprising within a molecule thereof, at least the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING;

a polypeptide comprising within a molecule thereof, at least a part or the whole of the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING that has varied or has been induced to vary;

a polypeptide comprising within a molecule thereof, at least the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING that has varied or has been induced to vary; or

a polypeptide comprising consecutive 100 amino acid residues having 30% or more homology with the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING.

[0024]

Also, the invention provides a recombinant plasmid comprising the polynucleotide encoding any of the following polypeptides:

a polypeptide comprising within a molecule thereof, at least a part or the whole of the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING;

a polypeptide comprising within a molecule thereof, at least the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING;

a polypeptide comprising within a molecule thereof, at least a part or the whole of the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING that has varied or has been induced to vary;

a polypeptide comprising within a molecule thereof, at least the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING that has varied or has been induced to vary; or

a polypeptide comprising consecutive 100 amino acid residues having 30% or more homology with the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING.

[0025]

In addition, the invention provides a recombinant microbial cell transformed with the aforementioned plasmid.

[0026]

The present invention will be described in details as follows.

[0027]

[Specific Modes of the Invention]

(Samples for Identification of Human Cyclin I)

The types of cells from which the human cyclin I according to this invention is derived for its identification, or isolation purposes may, although not particularly limited thereto, be skeletal muscle

cells, cultured fibroblasts or the like and cells derived from human cerebrum are most preferably used in the invention.

[0028]

Moreover, as to identification of human cyclin I it is possible to utilize various properties, in chemical structure or biochemical characteristics, which are generally known in cyclins and to use those as screening markers. Specifically, for this purpose cyclin's property of binding to specific Cdk can be used as a marker in a method such as the in vitro binding method (Matsu, Cell Engineering, 13, 528-533, 1994). Further, as it has been already documented, cyclin's property of complementing a yeast variant that has a deficiency in progression of its cell cycle can, for example, be used as a marker in the gene complement-screening method through introduction of genes (Lew et al., Cell, 6, 1197-1206, 1991). In this particular invention, whether or not a marker contains an amino acid sequence having a high degree of homology to the amino acid sequence referred to as " cyclin box" that is commonly found in the chemical structures of cyclins and is believed to play an important biochemical role can preferably be utilized to find a desirable marker for screening the cyclins. A variety of methods relying on the procedures

comparing with cyclins known in the art (e.g., judging significant differences based on calculation of homology to an amino acid sequence) can further be used to determine whether or not a marker has the cyclin box-like amino acid sequence, and they are not particularly limited in the invention.

[0029]

In addition, this invention places no particular limitation to the forms of samples for the aforementioned screening, and a usable method is to directly or indirectly identify and isolate polypeptides which posses the properties as described above employing the aforementioned properties and through suitable means: for example, it is the screening of an expression library by means of an antibody directed against the known cyclin box. Also, among others a method to screen and identify genes which encode the amino acid sequence from a suitable cDNA library is usable. In the invention, it is particularly preferred that a group of cDNAs selected from a suitable cDNA library through random sampling are taken as samples for screening.

[0030]

(Construction of cDNA Library)

In this invention, there is no particular limitation to selection of the aforementioned suitable

library and cDNA libraries available from various commercial sources and the like may preferably be used. The human cerebrum cDNA library that is available from various commercial sources is preferably usable in the invention. Furthermore, a normalized cDNA library can preferably be used in the invention: This library is, for example, obtained by the method of Sasaki et al., DNA Research 1, 91-96, 1994 (the content of each cDNA normalized).

[0031]

(Cloning of Human Cyclin I Gene cDNA)

In this invention, there is no particular limitation to the degree of cloning within the normalized human brain cDNA library thus obtained above. A suitable sampling method enables a part of the library to be selected. In the invention, about $1x10^3$-$5x10^3$ cDNA pieces may preferably be screened, for example.

[0032]

Further, there is no particular limitation to the techniques of obtaining plasmids during screening, and standard methods known in the art (e.g., Cell Engineering Experimental Protocol, Yamamoto et al. Ed., Shujun Publisher, 1991, pp 71-107) can be used. For example, enabling methods are a method to slice an insert by digestion with restriction enzymes followed

by incorporating the insert into a plasmid vector with the aid of ligase, an in vivo excision method using a helper phage, etc. In this invention, a plasmid may most preferably be converted to its form according to the in vivo excision method using the helper phage (i.e., the method described in the Uni-ZAP XR Cloning Kit Instruction Manual available from Stratagene Inc.).

[0033]

(Determination of Base Sequences)

While determination of the base sequence of the plasmid obtained above allows the selection of a gene encoding the cyclin box-like amino acid sequence as described above, whether to analyze a part or the whole of the insert is not particularly predetermined in this invention. According to the invention, it is possible to determine a base sequence with an appropriate length and then to select a suitable plasmid based on the results of the determination, which may be preferable. Namely, it is preferred in the invention that several base sequences at its 5'-end of the insert are determined, amino acid sequences to be encoded are predicted from the determined base sequences, and then a plasmid is selected based on the foregoing results. In this instance, preferably at least 200 bases are to be analyzed at its 5'-end of the insert. This is because this order of base number

is needed for the determination of homology to the cyclin box.

[0034]

In this invention, there is no particular limitation to the method for determining the base sequence at its 5'-end of the plasmid thus selected (not particularly limited and a suitable number at random may be selected, for example) and methods known in the art can be used. For example, the method relying on Taq cycle-sequencing (Biotechniques, 7, 494-499, 1989) can most preferably be used.

[0035]

Furthermore, there is no particular limitation to the method for comparing the amino acid sequence derived from the base sequence thus obtained with the cyclin proteins known already and a homology analysis according to standard methods is possible. For example, the homology analysis has been enabled by employing a commercial program (e.g., GENETYX program (Ver. 27, Software Development Co.)) and a protein data base (e.g., Protein Database (NBRF, Release 43)). As a result of this homology analysis, it will become possible to select those comprising consecutive 100 amino acid residues having 30% or more homology, for example.

[0036]

To thoroughly analyze the plasmid selected by the aforementioned method, screening methods for obtaining a clone containing the whole region that encodes the protein are not limited in this invention. It is preferred that the information on the base sequence at the 5'-end obtained as described above is utilized. There is no limitation as to whether a part or the whole of the base sequence is utilized in this screening, but it is enough to be possible utilizing this base sequence for the screening. For example, it is possible to utilize an approximately half of the base sequence obtained as described above. This also depends on the screening method to be used.

[0037]

As to the screening method, a variety of methods known in the art can preferably be used and they are not particularly limited. Specifically, the most preferred usable methods are a hybridization method using a labeled oligonucleotide, a RACE method using a primer along the 5'- or 3'-direction, etc. In this invention, it is particularly preferred that a labeled oligonucleotide having a base sequence which corresponds to about a half of the base sequence obtained as described above is used as a probe to perform screening through hybridization. There is no particular limitation to the aforementioned label and,

for example, [α- ^{32}P] dCPT, digoxigenin and the like can preferably be used. In addition, among others the hybridization conditions are not particularly limited and a variety of conditions previously known in the art can preferably be used in the invention (e.g., Cell Engineering Experimental Protocol, Yamamoto et al. Ed., Shujun Publisher, 1991, pp. 57-65).

[0038]

In this invention, there is no particular limitation to the methods for determining the base sequence of the insert from a positive clone screened as described above and a variety of methods known in the art are usable. For example, it is possible to use the method where deficient variants are prepared, the base sequences of individual clones determined, and on that basis ligation is achieved.

[0039]

A variety of methods known in the art as has been described already can be used to determine the base sequence of the longest insert among the inserts obtained as described above and, for example, one of them is a method where sequence primers are successively prepared from segments the amino acid sequences of which have been determined and they are read.

[0040]

(The Determined Human Cyclin I Gene Base Sequence)

The polynucleotide containing a part or the whole of the base sequence of a polynucleotide encoding the determined human cyclin I polypeptide is represented by Formula (2) (SEQ ID NO: 2 in SEQUENCE LISTING).

[0041]

Formula (2)

The aforementioned polynucleotides according to this invention encompass a polynucleotide comprising a base sequence which is the base sequence represented by Formula (2) and having no ATG bonded at its 5'-end.

[0042]

The polynucleotides of the invention also encompass DNA including 5'-flanking polynucleotides.

[0043]

Also, it is possible to vary a part of the structures of polynucleotides and deduced polypeptides therefrom without altering their principal activities (e.g., to activate phosphorylation) by means of natural or artificial mutation.

[0044]

Consequently, the polynucleotides according to the invention can possibly include base sequences encoding polypeptides which have structures of analogous isomers, variants or mutants of all the polypeptides as described above.

[0045]

Furthermore, it is possible to substitute at least one base of the base sequence of a polynucleotide with other kinds of bases without altering the amino acid sequence of a polypeptide produced by the polynucleotide in accordance with degeneracy in genetic codes. Hence, the polynucleotides of this invention can also possibly contain the base sequences converted by substitutions based on the degeneracy in genetic codes. In this case, the amino acid sequence deduced from the base sequence which has been obtained by the aforementioned substitution accords with the amino acid sequence of Formula (1) defined above.

[0046]

(The Amino Acid Sequence of Human Cyclin I)

Following Formula (1) (SEQ ID NO: 1 in SEQUENCE LISTING) represents the amino acid sequence of the human cyclin I polypeptide which is presumed based on the polynucleotide encoding the human cyclin I polypeptide the amino acid sequence of which has been determined according to the methods as explained above.

[0047]

Formula (1)

The amino acid sequences according to this invention encompass a polypeptide which is derived

from the aforementioned amino acid sequence having no methionine bonded at its N-terminal.

[0048]

Also, it is possible to vary a part of the structure of polynucleotides encoding polypeptides without altering their principal activities by means of natural or artificial mutation (e.g., Molecular Cloning, A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, 15.1-15.113, 1989) and the human cyclin I polypeptides according to the invention encompass polypeptides which have structures corresponding to analogous isomers, variants or mutants with the amino acid sequences as described above.

[0049]

(The Characteristics of Cyclin)

As shown in FIG. 2, the amino acid sequence translated from the determined base sequence displays significant homology to members of the already known cyclin family with respect to their cyclin boxes. Particularly, 41% homology is observed against rat cyclin G (Tamura et al., Oncogene, 8, 2113-2118, 1993) and 36% homology also observed against human cyclin E. Since the known cyclin members are referred to as " cyclins A-H" in the order of their identification, this novel cyclin will be referred to as " cyclin I."

As shown in FIG. 2, cyclin I identified in the invention displays significant homology to other members of the cyclin family within the region of cyclin boxes.

[0050]

By analogy to biological functions of the known members, it is expected that the cyclin I protein identified in this invention is able to bind to specific members of cdks which are kinds of kinase through its cyclin box and has the function of activating the kinase. Furthermore, according to conventional techniques known in the art such as antisense, it is possible to find a means to effectively inhibit synthesis of the human cyclin I protein and to provide a method for treating diseases in which the aforementioned kinase enzymes play an important role.

[0051]

(Transformed *E. coli* Containing Cyclin I)

Following the PCR method (Michael A. Innis et al. Ed., T. Saito Rev., PCR Experimental Manual, HBJ Press, 1991), only the region encoding proteins can be amplified from the clone obtained as described above which has the longest insert cDNA (about 1.7kb insert), and can be inserted into the EcoRI site of PCRII plasmid (Invitrogen Inc.). Although in this case the

primers to be used are not particularly limited in the invention, (ORF-s) CGTTCCCGGGTATGAAGTTTCCAGGGCCTTTGG and (ORF-AS) ACGGCTCGAGCTACATGACAGAAACAGGCTG are most preferably usable. Amplification under the known conditions (e.g., employing a DNA thermal cycler (Perkin Elmer Cetus Inc.) or the like) allows the region encoding proteins to be obtained. To insert this PCR fragment into a suitable plasmid such as the ECoRI site of pCRII plasmid, known methods (e.g., employing a TA cloning kit (Invitrogen Inc.) and following its attached operating instructions) can be used.

[0052]

According to the aforementioned procedures, it is possible to obtain transformed *E. coli* containing plasmid pCRII-cyclin I and, if necessary, this transformant will possibly be furnished from the strain deposited in the National Institute of Bioscience and Human-Technology, Agency of Industrial Science and Technology (Accession No. FERM P-15166).

[0053]

(Large Scale Production of Recombinant Cyclin Protein)

It is possible to insert into a suitable vector (e.g., between SmaI site and XhoI site within a pGEX-4T-1 vector (Pharmacia Inc.)), the PCR fragment comprising only the region that encodes the

aforementioned cyclin I protein; to grow *E. coli* cells containing the resulting plasmid under standard conditions; then to induce expression of the recombinant cyclin I protein (e.g., by using IPTG (Sima Inc.))(in this case, the protein is formed as a protein fused with GST protein); and to recover the recombinant cyclin I protein from the cells. This procedure can be performed according to conventionally known methods such as a modification of the method described in the instruction manual of pGEX-4T-1 vector (Pharmacia Inc.). Thus, it has become possible to produce the cyclin I protein in large quantities.

[0054]

(Cyclin I as Neuron Marker)

The present inventor has investigated as to which brain cells the cyclin I protein according to this invention is abundant in, and as a result, discovered that the protein is mostly localized in neuron. Based on this finding, the present inventor has found a method to specifically detect neuron by means of the cyclin I protein and the cyclin I gene according to the invention. An embodiment of the invention is described below.

[0055]

For example, (1) a brain section sample in appropriate thickness is prepared using a cryostat

(Hacker Instruments Inc.) and placed on a slide glass coated with gelatin; and then (2) the section is appropriately treated (e.g., postfixing, acetylation, and dehydration according to a modification of the method by Himi et al., Neuroscience, 60, 907-926, 1994); and hybridization is further performed using a probe labeled with a suitable labeling agent (e.g., digoxigenin).

[0056]

An antisense probe of cyclin I is prepared by performing in vitro transcription with T3RNA polymerase (Biolabs Inc.) in the presence of digoxigenin-labeled UTP (Boehringer Inc.) after digestion of the plasmid containing cyclin I cDNA with a suitable restriction enzyme that cleaves only the 5'-end of the cDNA followed by its ring-opening. Further, an antisense probe of SCG10 which is to be used as a positive control for the neuron marker is prepared in like manner; for example it is possible according to a modification of the method by Himi et al., as described in Neuroscience, 60, 907-926, 1994.

[0057]

(3) In situ hybridization, RNAse treatment, and washing can be performed according to a method known in the art such as the method by Himi et al., Neuroscience, 60, 907-926, 1994. Subsequently, after

the section is treated with a blocking agent (DIFCO Inc.), it is incubated with an anti-digoxigenin-alkaline phosphatase labeled antibody (Boehringer Inc.). Signals are detected by chromophoric visualization using NBT (nitroblue tetrazolium salt) and X-phosphate toluidium salt, both of which are available from Boehringer Inc.

[0058]

As the results are shown in FIG. 3, the hippocampus where neurons are concentrated gives clear signals. In FIG. 3-2 the cyclin I gene and a rat brain section neighboring on the hippocampus were used. Both FIG. 3-1 and FIG. 3-2 show clear signals at completely identical sites, where neurons are localized.

[0059]

Consequently, any base sequence complementary to a partial or the whole base sequence of the cyclin I gene finds value as a neuron marker. For example, it can be utilized to find the sites of neuron in a brain section during research or clinical investigations.

[0060]

(Preparation of Anti-Cyclin I Antibodies and Method for the Detection of Cyclin I Protein)

The preparation of an antibody can be performed using a part or the whole of a peptide comprising the

amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING, or the purified cyclin I protein according to the method as described in Chapter 5, " Antibodies; A Laboratory Manual" (Cold spring Harbor Laboratory Press, 1988). For example, procedures known in the art can be used to immunize rabbits and to provide antisera.

[0061]

According to western blotting employing the antisera prepared as described above, detection and identification of the cyclin I protein has been enabled. Specifically, a sample containing the cyclin I protein is charged on an acrylamide gel and allowed to react with the aforementioned antisera, which enables the detection of a band at a 43kDa position (which corresponds to the polypeptide having SEQ No. 1 in SEQUENCE LISTING). The foregoing manipulations can be performed according to conventional methods known in the art, such method as described in Chapter 12, " Antibodies; A Laboratory Manual" (Cold Spring Harbor Laboratory Press, 1988).

[0062]

(Control of the Biosynthesis of Cyclin I Protein by an Antisense Nucleotide)

An antisense nucleotide which are useful in this invention to control or inhibit the biosynthesis of

cyclin I protein can be selected by means known in the art and, for example, that with desired structure is available through a chemical synthesis (e.g., Takeuchi et al., Experimental Medicine, 12,1657-1663, 1994). Also, it can be provided by the method where an antisense segment is incorporated into a suitable vector such as pCMV1 and expressed in a cell; for example, it is possible according to a modification of the method by Kobayashi et al. as described in Antisense Research and Development, 5, 141-148, 1995.

[0063]

A nucleotide sequence to be usable includes an antisense polynucleotide corresponding to a polynucleotide having a part or the whole of the base sequence set forth in SEQ ID NO: 2 in SEQUENCE LISTING, said antisense polynucleotide controlling the biosynthesis of any of the following polypeptides forming a complex with kinase and controlling the activity of the kinase:

a polypeptide comprising within a molecule thereof, at least a part or the whole of the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING;

a polypeptide comprising within a molecule thereof, at least the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING;

a polypeptide comprising within a molecule thereof, at least a part or the whole of the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING that has varied or has been induced to vary;

a polypeptide comprising within a molecule thereof, at least the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING that has varied or has been induced to vary; or

a polypeptide comprising consecutive 100 amino acid residues having 30% or more homology with the amino acid sequence set forth in SEQ ID NO: 1 in SEQUENCE LISTING. In addition, the aforementioned polynucleotide that has varied or has been induced to vary is also usable.

[0064]

For administration or incorporation to cells, in the case of an oligonucleotide it is enabled by the method by Takeuchi et al. as described in Experimental Medicine, 12, 1657-1663, 1994; in the case of use of an expression vector, it is enabled by the method by Kobayashi et al. as described in Antisense Research and Development, 5, 141-148, 1995.

[0065]

Having controlled or inhibited the biosynthesis of the cyclin I protein intracellularly, the antisense nucleotides of the invention can be used in the

following: (i) an effective reagent or method for analyzing intracellular physiological effects of cyclin I; or (ii) an effective reagent or method for studying influences which cyclin I, being excessively present within the cells, has on said cells, tissues, or a living body, in which case they are made applicable to therapeutic agent for removing or alleviating undesirable influences or the like caused by cyclin I's excessiveness.

[0066]

The abbreviations used herein to describe the invention are tabulated below:

[0067]

Abbreviations

DNA	Deoxyribonucleic acid
A	Adenine
C	Cytosine
G	Guanine
T	Thymine
Ala (A)	Alanine
Arg (R)	Arginine
Asn (N)	Asparagine
Asp (D)	Aspartic acid
Cys (C)	Cystine
Gln (Q)	Glutamine
Glu (E)	Glutamic acid

Gly (G)	Glycine
His (H)	Histidine
Ile (I)	Isoleucine
Leu (I)	Luecine
Lys (K)	Lysine
Met (M)	Methionine
Phe (F)	Phenylalanine
Pro (P)	Proline
Ser (S)	Serine
Thr (T)	Threonine
Trp (W)	Tryptophan
Tyr (Y)	Tyrosine
Val (V)	Valine

[0068]

[Examples]

Although this invention is concretely illustrated by way of examples, it is not limited to the following examples insofar as it does not depart from its essence.

[0069]

EXAMPLE 1

Construction of Human Brain-derived Normalized cDNA Library

The normalized cDNA library was constructed using mRNA derived from a human cerebrum. According to the method of Sasaki, et al., DNA Research 1, 91-96,

1994, step (i)-selfhybridization in a semisolid system, step (ii)-construction of a phage cDNA library from the mRNA treated in step (i), and step (iii)-conversion of insert cDNA into cRNA were carried out in a sequence of (i)(ii)(iii)(i)(ii) and the normalized cDNA library was constructed.

[0070]

Cloning of Human Cyclin I Gene cDNA

(1) One hundred μL out of 1 mL of the normalized cDNA library constructed by the aforementioned method was converted into a plasmid form according to the *in vivo* excision method (as described in the Uni-Zap XR Cloning Kit Instruction Manual available from Stratagene Inc.) employing a helper phage (EXAssist available from Stratagene Inc.).

[0071]

More specifically, 200 μL of *E. coli* XL-1 Blue, 100 μL of the normalized cDNA library, and 1 μL of helper phage R408 (>1×10^6 pfu/ml) were mixed in a 50 mL test tube and the ZAP was allowed to be transfected by the helper phage at 37 °C for 15 minutes.

[0072]

To the mixture was added 5 mL of a 2xYT medium (10 g NaCl, 10 g Bacto Yeast Extract, and 16 g Bactotryptone/1L) and it was incubated under shaking at 37 °C for 3 hours to have phagemid excreted from *E.*

coli.

[0073]

After heat-treatment at 70°C for 20 minutes, the culture was centrifugated at 4000 g and the cells were destroyed. The supernatant phagemid was transferred to a different test tube.

[0074]

This supernatant contained pBluescript SK(-) particles, and 200 μL of the supernatant or 20 μL of its 100 times dilution and 200 μL of XL-1 Blue (OD 600 =1.0) were mixed at 37°C for 15 minutes to induce transfection.

[0075]

After plating 1-100 μL of the cultured solution on a LB/Amp plate, it was incubated overnight at 37°C. Colonies that appeared were *E. coli* (XL-1 Blue) transformants which had double-stranded pBluescript SK(-) containing insert DNA.

[0076]

(2) A plasmid was prepared from the aforementioned *E. Coli* using a QIAwell 8 Plus kit (Qiagen Inc.).

[0077]

(3) The base sequence at its 5'-end of the insert DNA of the thus obtained plasmid was determined on an autosequencer 373A (Perkin Elmer) using the Taq cycle-

sequencing method (Biotechniques, 7, 494-499, 1989).

[0078]

(4) The amino acid sequence obtained by translation of the thus determined base sequence was compared with a protein database (NBRF, Release 43) by use of the GENETYX Program (Ver. 27 available from Software Development Inc.) to carry out homology analysis.

[0079]

(5) More than 500 plasmids were subjected to the sequence determination and homology analysis to select the one that had an amino acid sequence like the cyclin box (named FC6 where "FC" is the abbreviation of Forebrain Cortex). To analyze it further in detail, a clone containing the whole region that encodes the protein was prepared by the procedures described below.

[0080]

(6) With cDNA library derived from temporal lobe cortex (Stratagene Inc.), screening was performed using the 5'-end half of the aforementioned FC6 clone as a probe.

[0081]

Twenty μL of the phage library solution and 200 μL of *E. coli* XL-1 Blue were incubated at 37°C for 15 minutes. This culture was added to 2-3 mL of top-agar (48°C), the mixture was plated on six NZY agar plate,

and was grown overnight at 37°C.

[0082]

Approximately the number of 50,000 of plaque were cultured on a 100 mm square plate. Therefore, the number of ca. $3x10^5$ of plaque were cultured on 6 plates and used for screening.

[0083]

The NZY plate was cooled at 4°C for two hours and a nylon filter (High Bond N+; available from Amasham Inc.) was placed over the plate and allowed to stand for two minutes.

[0084]

This filter was peeled off, dried on a filter paper, and the plaques were fixed under the ultraviolet irradiation to prepare a screening filter.

[0085]

Hybridization was performed according to the procedures as described below.

[0086]

The probe for use in hybridization was the one that had been obtained by labeling the 5`-end half of FC6 clone with ^{32}P-dCTP using a Megaprime Labeling Kit (Amasham Inc.).

[0087]

A mixture of 5xSSC (NaCl 0.15 M, sodium citrate (pH 7.0) 0.015 M), 50% formamide 1xdenhardt solution

(bovine serum albumin (Fraction V) 0.2% poly(vinylpyrolidone) 0.2%, and Ficoll400 0.2%), 0.1% SDS, and 100 μg/mL of salmon sperm DNA was used as a prehybridization solution.

[0088]

The filter was first incubated in the prehybridization solution at 42°C for three hours, and then in a hybridization solution to which the labeled probe had been added, at 42°C for 16 hours to effect hybridization.

[0089]

Following the aforementioned manipulations, three positive clones were obtained. The centers of plaques of the resulting positive ZAP phage clones on the agar plates were scooped out with a Pasteur pipette and the clones were eluted in a mixed solution of 500 μL of SM buffer and 20 μL of chloroform, and were allowed to stand overnight after having been vortexed.

[0090]

Two hundred μL of *E. coli* XL-1 Blue, 200 μL of the positive phage clone (>1x10^5 pfu/ml phage particles), and one μL of helper phage R408 (>1x10^{6}pfu/ml) were mixed in a 50 mL test tube and the ZAP was allowed to be transfected by the helper phage at 37°C for 15 minutes.

[0091]

To the mixture was added 5 mL of the 2xYT medium (10 g NaCl, 10 g Bacto Yeast Extract, and 16 g Bactotryptone/1L) and it was incubated under shaking at 37°C for 3 hours to have phagemid excreted from *E. coli*. After heat-treatment at 70°C for 20 minutes, the culture was centrifuged at 4,000 g and the cells were destroyed. The supernatant phagemid was transferred to another test tube.

[0092]

This supernatant contained pBluescript particles, and 200 μL of the supernatant or 20 μL of its 100 times dilution and 200 μL of XL-1 Blue (OD 600=1.0) were mixed at 37 °C for 15 minutes to induce transfection.

[0093]

After plating 1-100 μL of the cultured solution on a LB/Amp plate, it was incubated overnight at 37°C. Colonies that appeared were *E. coli* (XL-1 Blue) transformants which had double-stranded pBluescript SK(-) containing insert DNA.

[0094]

Plasmids were prepared from the three positive *E. coli* clones using a QIAprepPlasmid Kit (Qiagen Inc.) and among them, the clone that had the longest insert DNA (about 1.7kb insert) was subjected to the DNA base sequencing as described below.

[0095]

(7) The base sequence of the thus obtained 1.4k clone was determined on an autosequencer 373A (Perkin Elmer) using the Taq cycle-sequencing method (Biotechniques, 7, 494-499, 1989). Based on the results of the cDNA base sequence analysis for the resulting human cyclin I, 1328 bases are shown in FIG. 1. The open reading frame of the human cyclin I is comprised of 1134 bases, which encode 377 amino acids.

[0096]

Sequence Analysis of Amino Acids Encoded by Human Cyclin I Gene

As shown in FIG. 2, the amino acid sequence translated from the determined base sequence displays significant homology to members of the already known cyclin family with respect to their cyclin boxes. Particularly, 41% homology is observed against rat cyclin G (Tamura, et al., Oncogene, 8, 2113-2118, 1993) and 36% homology also observed against human cyclin E. Since the known cyclin members are referred to as " cyclins A-H" in the order of their identification, this novel cyclin will be referred to as " cyclin I." As shown in FIG. 2, cyclin I identified in the invention displays significant homology to other members of the cyclin family within the region of cyclin boxes.

[0097]

EXAMPLE 2

Following the PCR method (Michael A. Innis, et al., Ed., T. Saito Rev., PCR Experimental Manual, HBJ Press, 1991), only the region encoding proteins was amplified from the clone prepared according to Example 1 which had the longest insert cDNA (about 1.7kb insert).

[0098]

The primers for use were as follows:

(ORF-s) CGTTCCCGGGTATGAAGTTTCCAGGGCCTTTGG; and

(ORF-AS) ACGGCTCGAGCTACATGACAGAAACAGGCTG

[0099]

With the use of the primer concentrations of 20 pmol/μL and 0.025 U /μL of Taq DNA polymerase at three cycles, a DNA thermal cycler (Perkin Elmer (Cetus)Inc.) was employed to do amplification and to obtain the region that encodes the protein.

[0100]

To insert this PCR fragment into the EcoRI site of the pCRII plasmid, a TA cloning kit (Invitrogen Inc.) was employed following its attached operating instructions. Transformed *E. coli* containing plasmid pCRII-cyclin I prepared according to the method as described above was designated as pCRII-cyclin I and deposited on September 8, 1995 in the National

Institute of Bioscience and Human-Technology, Agency of Industrial Science and Technology (Accession No. FERM P-15166).

[0101]

EXAMPLE 3

Investigation on Applicability of Cyclin I as Neuron Marker

(1) Brain sections from adult male rats (Sprague-Dawley, three months old) in a thickness of 13 microns were prepared using a cryostat (Hacker Instruments Inc.) and placed on slide glasses coated with gelatin.

[0102]

(2) According to the method by Himi, et al., Neuroscience, 60, 907-926, 1994, the section was subjected to postfixing, acetylation, and dehydration and then hybridization was performed using a probe labeled with digoxigenin.

[0103]

An antisense probe of cyclin I was prepared by performing the in vitro transcription with T3RNA polymerase (Biolabs Inc.) in the presence of digoxigenin-labeled UTP (Boehringer Inc.) after ring-opening of the aforementioned plasmid digesting the plasmid at XhoI. In like manner, an antisense probe of SCG10 which was to be used as a positive control for the neuron marker was prepared (Neuroscience, 60,

907-926, 1994).

[0104]

(3) In situ hybridization, RNAse treatment, and washing were performed according to the method by Himi, et al., Neuroscience, 60, 907-926, 1994. Subsequently, the section was treated with a blocking agent (DIFCO Inc.) and thereafter, was incubated with an anti-digoxigenin-alkaline phosphatase labeled antibody (Boehringer Inc.). Signals were detected by chromophoric visualization using NBT (nitroblue tetrazolium salt) and X-phosphate toluidium salt, both of which were available from Boehringer Inc. FIG. 3 illustrates the results.

[0105]

Here, the hippocampus where neurons are concentrated gives clear signals. In FIG. 3-2 the cyclin I gene and a rat brain section neighboring on the hippocampus were used. Both FIG. 3-1 and FIG. 3-2 show clear signals at completely identical sites, where neurons are localized. Consequently, any base sequence complementary to a partial or the whole base sequence of the cyclin I gene finds value as a neuron marker. For example, it can be utilized to find the sites of neuron in a brain section during research or clinical investigations.

[0106]

EXAMPLE 4

Large Scale Production of Recombinant Cyclin Protein

(1) The PCR fragment prepared according to Example 2 and which comprised only the region that encodes the protein was inserted between SmaI site and XhoI site within a pGEX-4T-1 vector (Pharmacia Inc.).

[0107]

(2) *E. coli* cells containing the resulting plasmids were grown, then expression of the recombinant cyclin I protein was induced by IPTG (Sima Inc.), in which case the protein was formed as a protein fused with GST protein, and the recombinant cyclin I protein was recovered from the cells. The foregoing procedure was performed according to the method described in the instruction manual of pGEX-4T-1 vector (Pharmacia Inc.).

[0108]

EXAMPLE 5

Preparation of Anti-Cyclin I Antibodies

(1) The preparation of the antibodies was performed using the recombinant cyclin I protein prepared according to Example 4 by following a modification of the method as described in Chapter 5, " Antibodies; A Laboratory Manual" (Cold Spring Harbor Laboratory Press, 1988).

[0109]

Rats were immunized in order to obtain antisera.

[0110]

(2) A solution extracted from TIG-1 cells containing the cyclin I protein was charged on an acrylamide gel and subjected to analysis by western blotting using the antiserum prepared according to Procedure (1), which detected a band corresponding to the cyclin I protein at a 43kDa position. The foregoing manipulations are performed according to the method as described in Chapter 12, " Antibodies; A Laboratory Manual" (Cold Spring Harbor Laboratory Press, 1988).

[0111]

SEQUENCE LISTING

SEQ ID NO: 1

LENGTH : 377

TYPE : amino acid

TOPOLOGY : linear

MOLECULE TYPE : peptide

SEQUENCE DESCRIPTION:

Met Lys Phe Pro Gly Pro Leu Glu Asn Gln Arg Leu Ser Phe Leu
5 10 15

Leu Glu Lys Ala Ile Thr Arg Glu Ala Gln Met Trp Lys Val Asn
20 25 30

Val Arg Lys Met Pro Ser Asn Gln Asn Val Ser Pro Ser Gln Arg
35 40 45

Asp Glu Val Ile Gln Trp Leu Ala Lys Leu Lys Tyr Gln Phe Asn
50 55 60
Leu Tyr Pro Glu Thr Phe Ala Leu Ala Ser Ser Leu Leu Asp Arg
65 70 75
Phe Leu Ala Thr Val Lys Ala His Pro Lys Tyr Leu Ser Cys Ile
80 85 90
Ala Ile Ser Cys Phe Phe Leu Ala Ala Lys Thr Val Glu Glu Asp
95 100 105
Glu Arg Ile Pro Val Leu Lys Val Leu Ala Arg Asp Ser Phe Cys
110 115 120
Gly Cys Ser Ser Ser Glu Ile Leu Arg Met Glu Arg Ile Ile Leu
125 130 135
Asp Lys Leu Asn Trp Asp Leu His Thr Ala Thr Pro Leu Asp Phe
140 145 150
Leu His Ile Phe His Ala Ile Ala Val Ser Thr Arg Pro Gln Leu
155 160 165
Leu Phe Ser Leu Pro Lys Leu Ser Pro Ser Gln His Leu Ala Val
170 175 180
Leu Thr Lys Gln Leu Leu His Cys Met Ala Cys Asn Gln Leu Leu
185 190 195
Gln Phe Arg Gly Ser Met Leu Ala Leu Ala Met Val Ser Leu Glu
200 205 210
Met Glu Lys Leu Ile Pro Asp Trp Leu Ser Leu Thr Ile Glu Leu
215 220 225
Leu Gln Lys Ala Gln Met Asp Ser Ser Gln Leu Ile His Cys Arg
230 235 240

Glu Leu Val Ala His His Leu Ser Thr Leu Gln Ser Ser Leu Pro
245 250 255
Leu Asn Ser Val Tyr Val Tyr Arg Pro Leu Lys His Thr Leu Val
260 265 270
Thr Cys Asp Lys Gly Val Phe Arg Leu His Pro Ser Ser Val Pro
275 280 285
Gly Pro Asp Phe Ser Lys Asp Asn Ser Lys Pro Glu Val Pro Val
290 295 300
Arg Gly Thr Ala Ala Phe Tyr His His Leu Pro Ala Ala Ser Gly
305 310 315
Cys Lys Gln Thr Ser Thr Lys Arg Lys Val Glu Glu Met Glu Val
320 325 330
Asp Asp Phe Tyr Asp Gly Ile Lys Arg Leu Tyr Asn Glu Asp Asn
335 340 345
Val Ser Glu Asn Val Gly Ser Val Cys Gly Thr Asp Leu Ser Arg
350 355 360
Gln Glu Gly His Ala Ser Pro Cys Pro Pro Leu Gln Pro Val Ser
365 370 375
Val Met

SEQ ID NO: 2

LENGTH : 1134

TYPE : nucleic acid

STRANDEDNESS : double

TOPOLOGY : linear

MOLECULE TYPE : DNA

SEQUENCE DESCRIPTION:

ATG AAG TTT CCA GGG CCT TTG CAA AAC CAG AGA TTG TCT TTC CTG 45

TTG GAA AAG GCA ATC ACT AGG GAA GCA CAG ATG TGG AAA GTG AAT 90

GTG CGG AAA ATG CCT TCA AAT CAG AAT GTT TCT CCA TCC CAG AGA 135

GAT GAA GTA ATT CAA TGG CTG GCC AAA CTC AAG TAC CAA TTC AAC 180

CTT TAC CCA GAA ACA TTT GCT CTG GCT AGC AGT CTT TTG GAT AGG 225

TTT TTA GCT ACC GTA AAG GCT CAT CCA AAA TAC TTG AGT TGT ATT 270

GCA ATC AGC TGT TTT TTC CTA GCT GCC AAG ACT GTT GAG GAA GAT 315

GAG AGA ATT CCA GTA CTA AAG GTA TTG GCA AGA GAC ACT TTC TGT 360

GGA TGT TCC TCA TCT GAA ATT TTG AGA ATG GAG AGA ATT ATT CTG 405

GAT AAG TTG AAT TGG GAT CTT CAC ACA GCC ACA CCA TTG GAT TTT 450

CTT CAT ATT TTC CAT GCC ATT GCA GTG TCA ACT AGG CCT CAG TTA 495

CTT TTC AGT TTG CCC AAA TTG AGC CCA TCT CAA CAT TTG GCA GTC 540

CTT ACC AAG CAA CTA CTT CAC TGT ATG GCC TGC AAC CAA CTT CTG 585

CAA TTC AGA GGA TCC ATG CTT GCT CTG GCC ATG GTT AGT CTG GAA 630

ATG GAG AAA CTC ATT CCT GAT TGG CTT TCT CTT ACA ATT GAA CTG 675

CTT CAG AAA GCA CAG ATG CAT AGC TCC CAG TTG ATC CAT TGT CCC 720

GAG CTT GTG GCA CAT CAC CTT TCT ACT CTG CAG TCT TCC CTG CCT 765

CTG AAT TCC GTT TAT GTC TAC CGT CCC CTC AAG CAC ACC CTG GTG 810

ACC TGT GAC AAA GGA GTG TTC AGA TTA CAT CCC TCC TCT GTC CCA 855

GGC CCA GAC TTC TCC AAG GAC AAC AGC AAG CCA GAA GTG CCA GTC 900

AGA GGT ACA GCA GCC TTT TAC CAT CAT CTC CCA GCT GCC AGT GGG 945

TGC AAG CAG ACC TCT ACT AAA CGC AAA GTA GAG GAA ATG GAA GTG 990

GAT GAC TTC TAT GAT GGA ATC AAA CGG CTC TAT AAT GAA GAT AAT 1035

GTC TCA GAA AAT GTG GGT TCT GTG TGT GGC ACT CAT TTA TCA AGA 1080

CAA GAG GGA CAT GCT TCC CCT TGT CCA CCT TTG CAG CCT GTT TCT 1125

GTC ATG TAG 1134

SEQ ID NO : 3

LENGTH : 33

TYPE : nucleic acid

STRANDEDNESS : double

TOPOLOGY : linear

MOLECULE TYPE : DNA

SEQUENCE LISTING

CGTTCCCGGG TATGAAGTTT CCAGGGCCTT TGG 33

SEQ ID NO : 4

LENGTH : 31

TYPE : nucleic acid

STRANDEDNESS : double

TOPOLOGY : linear

MOLECULE TYPE : DNA

SEQUENCE LISTING

ACGGCTCGAG CTACATGACA GAAACAGGCT G 31

[BRIEF DESCRIPTION OF DRAWINGS]

[FIG. 1]

FIG. 1 shows the base sequence of human cyclin I gene and its corresponding deduced amino acid sequence of human cyclin I protein.

[FIG. 2]

A comparison between the amino acid sequence of human cyclin I and the amino acid sequences of other members of the cyclin family is shown. (A) A comparison in the cyclin box (the blackened parts indicate consensus amino acids). (B) A comparison between human cyclin I and rat cyclin G (the underlined parts indicate the cyclin box).

[FIG. 3]

Photographs of localization of human cyclin I mRNA in neuron as determined by the in situ hybridization method using a rat brain section with the aid of an antisense cRNA probe are shown. Both A and F show a rat brain section centered at its hippocampus and A shows the results obtained using SCG10, while B shows those obtained using cyclin I antisense cRNA as a probe. Here, the parts visible in black are where neurons are concentrated. In the hippocampi (CA1, CA3, and DG), byramidal cells and granulocytes (both neurons) are strongly stained. DG represents " dentate gyrus," CA3 " Cajail's area 3," CTX " frontal cortex," CA1 " Cajail's area 1," and CP " choroid plexus."